

# IN THE SPECIFICATION

Please replace paragraph [0004] with the following replacement paragraph:

[0004] The CCHH class, typified by the *Xenopus* transcription factor IIIA (19), is the largest. These proteins contain two or more fingers in tandem repeats. In contrast, the steroid receptors contain only cysteine residues that form two types of zinc-coordinated structures with four (C<sub>4</sub>) and five (C<sub>5</sub>) cysteines (28). Another class of zinc fingers contains the CCHC fingers. The CCHC fingers, which are found in *Drosophila*, and in mammalian and retroviral proteins, display the consensus sequence ~~C-X<sub>2</sub>-C-X<sub>4</sub>-H-X<sub>4</sub>-C~~ C-N<sub>2</sub>-C-N<sub>4</sub>-H-N<sub>4</sub>-C (SEQ ID NO:65) (Refs. 7, 21, 24). Recently, a novel configuration of CCHC finger, of the ~~C-X<sub>5</sub>-C-X<sub>12</sub>-H-X<sub>4</sub>-C~~ C-N<sub>5</sub>-C-N<sub>12</sub>-H-N<sub>4</sub>-C (SEQ ID NO:66) type, was found in the neural zinc finger factor/myelin transcription factor family (Refs. 11, 12, 36). Finally, several yeast transcription factors such as GAL4 and CHA4 contain an atypical C<sub>6</sub> zinc finger structure that coordinates 2 zinc ions (Refs. 9, 32).

Please replace the Sequence Listing beginning on page 55 of the specification with the Substitute Sequence Listing Sheets, provided as Exhibit A hereto.